

#2

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/838,028

DATE: 05/08/2001

TIME: 15:55:54

Input Set : A:\00125US2.ST25.txt
Output Set: N:\CRF3\05082001\I838028.raw

ENTERED

3 <110> APPLICANT: Lind, Peter
 4 Berthold, Malin
 6 <120> TITLE OF INVENTION: Novel G Protein-Coupled Receptor
 8 <130> FILE REFERENCE: 00125US2
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/838,028
 C--> 10 <141> CURRENT FILING DATE: 2001-04-19
 10 <150> PRIOR APPLICATION NUMBER: 60/198,600
 11 <151> PRIOR FILING DATE: 2000-04-19
 13 <160> NUMBER OF SEQ ID NOS: 12
 15 <170> SOFTWARE: PatentIn version 3.0
 17 <210> SEQ ID NO: 1
 18 <211> LENGTH: 1540
 19 <212> TYPE: DNA
 20 <213> ORGANISM: Homo sapiens
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 29 tggggtcccg gaggtggggc tacgggatgt tgcttcggaa tctgtggccc tcttcttcat 240
 31 gctcctgtg gacttgactg ctgtggctgg caatggccgt gtgatggccg tgatgc当地 300
 33 gacgcctgccc ctccgaaaat ttgtcttcgt ctccacactc tgccctggg acctgtggc 360
 35 tgccctgacc ctcatgcccc tggccatgtc ctccagctct gcctctttt accacgc当地 420
 37 ctttggggag gtggcctgccc gcctctactt gtttctgagc gtgtgtttt tcagc当地 480
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 78 <212> TYPE: PRT
 79 <213> ORGANISM: Homo sapiens
 81 <400> SEQUENCE: 2
 83 Met Glu Ser Ser Pro Ile Pro Gln Ser Ser Gly Asn Ser Ser Thr Leu

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87	20	25	30	
89	Glu Val Gly Leu Arg Asp Val Ala Ser Glu Ser Val Ala Leu Phe Phe			
90	35	40	45	
92	Met Leu Leu Leu Asp Leu Thr Ala Val Ala Gly Asn Ala Ala Val Met			
93	50	55	60	
95	Ala Val Ile Ala Lys Thr Pro Ala Leu Arg Lys Phe Val Phe Val Phe			
96	65	70	75	80
98	His Leu Cys Leu Val Asp Leu Leu Ala Ala Leu Thr Leu Met Pro Leu			
99	85	90	95	
101	Ala Met Leu Ser Ser Ser Ala Leu Phe Asp His Ala Leu Phe Gly Glu			
102	100	105	110	
104	Val Ala Cys Arg Leu Tyr Leu Phe Leu Ser Val Cys Phe Val Ser Leu			
105	115	120	125	
107	Ala Ile Leu Ser Val Ser Ala Ile Asn Val Glu Arg Tyr Tyr Tyr Val			
108	130	135	140	
110	Val His Pro Met Arg Tyr Glu Val Arg Met Thr Leu Gly Leu Val Ala			
111	145	150	155	160
113	Ser Val Leu Val Gly Val Trp Val Lys Ala Leu Ala Met Ala Ser Val			
114	165	170	175	
116	Pro Val Leu Gly Arg Val Ser Trp Glu Glu Gly Ala Pro Ser Val Pro			
117	180	185	190	
119	Pro Gly Cys Ser Leu Gln Trp Ser His Ser Ala Tyr Cys Gln Leu Phe			
120	195	200	205	
122	Val Val Val Phe Ala Val Leu Tyr Phe Leu Leu Pro Leu Leu Ile			
123	210	215	220	
125	Leu Val Val Tyr Cys Ser Met Phe Arg Val Ala Arg Val Ala Ala Met			
126	225	230	235	240
128	Gln His Gly Pro Leu Pro Thr Trp Met Glu Thr Pro Arg Gln Arg Ser			
129	245	250	255	
131	Glu Ser Leu Ser Ser Arg Ser Thr Met Val Thr Ser Ser Gly Ala Pro			
132	260	265	270	
134	Gln Thr Thr Pro His Arg Thr Phe Gly Gly Lys Ala Ala Val Val			
135	275	280	285	
137	Leu Leu Ala Val Gly Gly Gln Phe Leu Leu Cys Trp Leu Pro Tyr Phe			
138	290	295	300	
140	Ser Phe His Leu Tyr Val Ala Leu Ser Ala Gln Pro Ile Ser Thr Gly			
141	305	310	315	320
143	Gln Val Glu Ser Val Val Thr Trp Ile Gly Tyr Phe Cys Phe Thr Ser			
144	325	330	335	
146	Asn Pro Phe Phe Tyr Gly Cys Leu Asn Arg Gln Ile Arg Gly Glu Leu			
147	340	345	350	
149	Ser Lys Gln Phe Val Cys Phe Phe Lys Pro Ala Pro Glu Glu Glu Leu			
150	355	360	365	
152	Arg Leu Pro Ser Arg Glu Gly Ser Ile Glu Glu Asn Phe Leu Gln Phe			
153	370	375	380	
155	Leu Gln Gly Thr Gly Cys Pro Ser Glu Ser Trp Val Ser Arg Pro Leu			
156	385	390	395	400

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161	Gln	Ile	Ala	Glu	Glu	Thr	Ser	Glu	Phe	Leu	Glu	Gln	Gln	Leu	Thr	Ser	
162					420				425							430	
164	Asp	Ile	Ile	Met	Ser	Asp	Ser	Tyr	Leu	Arg	Pro	Ala	Ala	Ser	Pro	Arg	
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180	catcaggaaa	ctcatccact	ttggaaaggg	cccttcaaacc	cccaggcccc	tctacggcca										180	
182	gcggagtc	agagttggga	ctaaggacg	tggcttcgg	atctgtggcc	cttttcttca										240	
184	tgttctgtt	ggatctca	gtgtggcg	gcaatgctgc	tgtgatggct	tttattggca										300	
186	agacaccgc	cctccgaaag	tttgggggg	tcttccatct	ctgtctgg	gacctgctgg										360	
188	ctgcccgtac	cctcatggcc	ctggccatgc	tctccagctc	tgccctctt	gaccacgccc										420	
190	tcttgggg	ggtggcctgc	cgcccttacc	tgttccctgag	cggttgc	gtcagcctgg										480	
192	ccatccccc	ggtgtctgcc	attaatgtgg	agcgctacta	ttatgtggc	cacccatgc										540	
194	gctacgaggt	gcgcatgaca	ctaggctgg	tggctctgt	gctgggggc	gtgtggtaa										600	
196	aggccctggc	catggcgct	gtgcccgt	ttggaaagggt	ctactggag	gaaggagctc										660	
198	ccagtgttaa	cccaggctgt	tctctccat	ggagccata	tgcctactgc	cagcttttg										720	
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208	tcctggctgt	cggggacag	ttcttgc	gttgttacc	ctacttct	ttccatct										1020	
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214	ggggcagct	tagcaaacag	tttgtctgtt	tctcaaggc	agctccagag	gaggagctg										1200	
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220	actttcaat	cccaggccag	attgtcgagg	agacctcg	tttcttgg	cagcaactca										1380	
222	ccagcgacat	catcatgtcg	gacagctacc	tccgtcctgc	cccttccacca	aggctgg										1440	
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232	gttgacaaag	gtgagggaaa	gccttctac	cagtgaact	ttcgtgc	aggagacagg										1740	
234	gcaacttctg	gttaggcatt	ggagcagcag	gttaggagca	tttattctgg	ggaccgttga										1800	
236	gttttacttc	tttccagttt	catagtc	actaatattt	atactgagac	aaggtaagaa										1860	
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246 <400> SEQUENCE: 4
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 255 35 40 45
 257 Met Leu Leu Leu Asp Leu Thr Ala Val Ala Gly Asn Ala Ala Val Met
 258 50 55 60
 260 Ala Val Ile Ala Lys Thr Pro Ala Leu Arg Lys Phe Val Phe Val Phe
 261 65 70 75 80
 263 His Leu Cys Leu Val Asp Leu Leu Ala Ala Leu Thr Leu Met Pro Leu
 264 85 90 95
 266 Ala Met Leu Ser Ser Ala Leu Phe Asp His Ala Leu Phe Gly Glu
 267 100 105 110
 269 Val Ala Cys Arg Leu Tyr Leu Phe Leu Ser Val Cys Phe Val Ser Leu
 270 115 120 125
 272 Ala Ile Leu Ser Val Ser Ala Ile Asn Val Glu Arg Tyr Tyr Tyr Val
 273 130 135 140
 275 Val His Pro Met Arg Tyr Glu Val Arg Met Thr Leu Gly Leu Val Ala
 276 145 150 155 160
 278 Ser Val Leu Val Gly Val Trp Val Lys Ala Leu Ala Met Ala Ser Val
 279 165 170 175
 281 Pro Val Leu Gly Arg Val Tyr Trp Glu Glu Gly Ala Pro Ser Val Asn
 282 180 185 190
 284 Pro Gly Cys Ser Leu Gln Trp Ser His Ser Ala Tyr Cys Gln Leu Phe
 285 195 200 205
 287 Val Val Val Phe Ala Val Leu Tyr Phe Leu Leu Pro Leu Ile Leu Ile
 288 210 215 220
 290 Phe Val Val Tyr Cys Ser Met Phe Arg Val Ala Arg Val Ala Ala Met
 291 225 230 235 240
 293 Gln His Gly Pro Leu Pro Thr Trp Met Glu Thr Pro Arg Gln Arg Ser
 294 245 250 255
 296 Glu Ser Leu Ser Ser Arg Ser Thr Met Val Thr Ser Ser Gly Ala His
 297 260 265 270
 299 Gln Thr Thr Pro His Arg Thr Phe Gly Gly Lys Ala Ala Val Val
 300 275 280 285
 302 Leu Leu Ala Val Gly Gly Gln Phe Leu Leu Cys Trp Leu Pro Tyr Phe
 303 290 295 300
 305 Ser Phe His Leu Tyr Val Ala Leu Ser Ala Gln Pro Ile Ser Thr Gly
 306 305 310 315 320
 308 Gln Val Glu Asn Val Val Thr Trp Ile Gly Tyr Phe Cys Phe Thr Ser
 309 325 330 335
 311 Asn Pro Phe Phe Tyr Gly Cys Leu Asn Arg Gln Ile Arg Gly Glu Leu
 312 340 345 350
 314 Ser Lys Gln Phe Val Cys Phe Phe Lys Ala Ala Pro Glu Glu Glu Leu
 315 355 360 365
 317 Arg Leu Pro Ser Arg Glu Gly Ser Ile Glu Glu Asn Phe Leu Gln Phe
 318 370 375 380

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320 Leu Gln Gly Thr Ser Glu Asn Trp Val Ser Arg Pro Leu Pro Ser Pro
321 385 390 395 400
323 Lys Arg Glu Pro Pro Pro Ala Val Asp Phe Arg Ile Pro Gly Gln Ile
324 405 410 415
326 Ala Glu Glu Thr Ser Glu Phe Leu Glu Gln Gln Leu Thr Ser Asp Ile
327 420 425 430
329 Ile Met Ser Asp Ser Tyr Leu Arg Pro Ala Pro Ser Pro Arg Leu Glu
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332 Ser
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352 <213> ORGANISM: Artificial Sequence
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356 <223> OTHER INFORMATION: Primer
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365 <212> TYPE: DNA
366 <213> ORGANISM: Artificial Sequence
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377 <210> SEQ ID NO: 8
378 <211> LENGTH: 48
379 <212> TYPE: DNA
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393 <212> TYPE: DNA
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VERIFICATION SUMMARY

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Input Set : A:\00125US2.ST25.txt
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L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date